

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 1, 2001, 16:22:07 ; Search time 88.16 seconds
(without alignments)
27.919 Million cell updates/sec

Title: US-09-331-631A-38

Perfect score: 53
Sequence: 1 CXXXXXXXXXXXXXXXXCXXC 21

Scoring table: BLOSUM62PX
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_15:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_fodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	100.0	32	6	077490 galago ciras
2	53	100.0	32	6	077493 lemur catia
3	53	100.0	46	4	016861 homo sapien
4	53	100.0	58	5	090623 pacifastacu
5	53	100.0	62	10	09M402 glycine max
6	53	100.0	66	12	041097 paramacium
7	53	100.0	72	5	09V199 drosophila
8	53	100.0	73	5	062554 mytilus edu
9	53	100.0	73	5	062555 mytilus edu
10	53	100.0	74	5	09V1A1 drosophila
11	53	100.0	74	6	09N0X1 oryctolagus
12	53	100.0	81	4	016274 homo sapien
13	53	100.0	83	11	09J0M45 mus musculu
14	53	100.0	84	12	072913 miscanthus
15	53	100.0	84	12	067593 mesobuthus
16	53	100.0	90	5	077091 ovis aries
17	53	100.0	96	6	077729 caenorhabd1
18	53	100.0	98	5	094162 caenorhabd1
19	53	100.0	101	5	090341 paramacium

20	53	100.0	104	5	09NLE3 leishmania
21	53	100.0	105	5	09NMV2 leishmania
22	53	100.0	108	5	09VUN1 drosophila
23	53	100.0	110	4	014633 homo sapien
24	53	100.0	115	5	046202 drosophila
25	53	100.0	117	4	095176 homo sapien
26	53	100.0	118	11	002393 mus musculu
27	53	100.0	121	6	09RTG8 hylobates m
28	53	100.0	125	4	095177 homo sapien
29	53	100.0	125	5	09N327 caenorhabd1
30	53	100.0	131	5	09M3A7 drosophila
31	53	100.0	135	5	018158 caenorhabd1
32	53	100.0	137	5	018157 caenorhabd1
33	53	100.0	137	6	09RTG8 hylobates a
34	53	100.0	137	6	09RTG7 hylobates k
35	53	100.0	137	6	09RTG6 hylobates m
36	53	100.0	142	5	09RTU5 caenorhabd1
37	53	100.0	144	6	077494 tarsius ban
38	53	100.0	151	6	028576 ovis aries
39	53	100.0	152	5	09XVX3 caenorhabd1
40	53	100.0	153	6	09RTU2 hylobates a
41	53	100.0	153	6	09RTU1 hylobates m
42	53	100.0	153	6	09RTU0 hylobates k
43	53	100.0	153	6	09RTU9 hylobates m
44	53	100.0	153	6	028834 oryctolagus
45	53	100.0	154	12	084631 paramacium

ALIGNMENTS

RESULT 1					
077490	PRELIMINARY;	PRT;	32 AA.		
AC 077490;					
DT 01-NOV-1998 (TREMBlrel. 08, Created)					
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)					
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)					
DE D4 DOPAMINE RECEPTOR (D4DR) (FRAGMENT).					
OS Galago crassicaudatus (Thick-tailed galago) (Otollemur crassicaudatus).					
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC Mammalia; Eutheria; Primates; Strepsirhini; Galagonidae; Otollemur.					
OX NCBI_TaxID=9463;					
ON [1]					
RP SEQUENCE FROM N.A.					
RA Inoue-Murayama M., Takenaka O., Murayama Y.;					
RT "Origin and divergence of tandem repeats of primate D4 dopamine					
RT receptor genes."					
RL Primates 39:217-224(1998).					
DR EMBL; AB016199; BAA32037.1; -					
FT NON_TER 1 32					
FT NON_TER 32 32					
SQ SEQUENCE 32 AA; 3157 MW; F492F6F29C2C5CEC CRC64;					
Query Match	100.0%;	Score 53;	DB 6;	Length 32;	
Best local Similarity	19.0%;	Pred. No. 61;			
Matches 4;	Conservative 17;	Mismatches 0;	Indels 0;	Gaps 0;	
QY 1 CXXXXXXXXXXXXXXXXCXXC 21					
DB 10 CDDCPAPAGPSQDPCDDPC 30					
RESULT 2					
077493	PRELIMINARY;	PRT;	32 AA.		
ID 077493;					
AC 077493;					
DT 01-NOV-1998 (TREMBlrel. 08, Created)					
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)					
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)					
DE D4 DOPAMINE RECEPTOR (D4DR) (FRAGMENT).					
OS Lemur catia (Ring-tailed lemur).					

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Primates; Strepsirrhini; Lemniscidae; Lemur.
RN NCBI_TaxID=9447;
RP SEQUENCE FROM N.A.
RA Inoue-Murayama M., Takenaka O., Murayama Y.;
RT "Origin and divergence of tandem repeats of primate DA dopamine
receptor genes";
RL Primates 39:217-224(1998).
DR EMBL: AB016202; BAA32040.1; -.
FT NON_TER 1 1
FT NON_TER 32 32
SQ SEQUENCE 32 AA; 3023 MW; F46F7D481DAF917C CRC64;

Query Match 100.0%; Score 53; DB 6; Length 32;
Best Local Similarity 19.0%; Pred. No. 61;
Matches 4; Conservative 17; Mismatches 0; Indels 0; Gaps 0;

OY 1 CXXXCXXXXXXXXXXCXXC 21
ID 10 CGADCOPAPGPGCGPC 30

RESULT 3

ID Q16861 PRELIMINARY; PRT; 46 AA.
AC Q16861;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DT 01-AUG-1998 (TREMBLrel. 07, last annotation update)
DE CYSTEINE-RICH PROTEIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
RN NCBI_TaxID=9606;
RP SEQUENCE FROM N.A.
RA Lemasson I., Devaux C., Mesnard J.M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U63332; AAB05810.1; -.
FT NON_TER 1 1
FT NON_TER 46 AA; 5061 MW; 311922FE40A4E8F CRC64;
SQ SEQUENCE 46 AA; 5061 MW; 311922FE40A4E8F CRC64;

Query Match 100.0%; Score 53; DB 4; Length 46;
Best Local Similarity 19.0%; Pred. No. 75;
Matches 4; Conservative 17; Mismatches 0; Indels 0; Gaps 0;

OY 1 CXXXCXXXXXXXXXXCXXC 21
ID 11 CCCCCCCCCCCCCCCCCC 31

RESULT 4

ID Q90623 PRELIMINARY; PRT; 58 AA.
AC Q90623;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, last annotation update)
DE METALLOTHIONEIN.
OS Pacifastacus leniusculus (Signal crayfish).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Astacoidae; Astacidae; Pacifastacus.
OX NCBI_TaxID=6720;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THORACIC GANGLIA;
RA Skorupski P., Dawbarn D.;
RT Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF199482; AAF07215.1; -.

DR HSP: P55949; IDMC.
DR INTERPRO: IPR002045; -.
DR INTERPRO: IPR003019; -.
DR PFAM: PF00131; metalchio.1.
DR PRINTS: PR00858; MTCRUSTACEAN.
SQ SEQUENCE 58 AA; 6008 MW; 576635ACB0E5100 CRC64;

Query Match 100.0%; Score 53; DB 5; Length 58;
Best Local Similarity 19.0%; Pred. No. 86;
Matches 4; Conservative 17; Mismatches 0; Indels 0; Gaps 0;

OY 1 CXXXCXXXXXXXXXXCXXC 21
ID 34 CTSCKCKPSKEDCAKTSKPC 54

RESULT 5

ID Q9M402 PRELIMINARY; PRT; 62 AA.
AC Q9M402;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, last annotation update)
DE ALPHA-TYPE BETA-CONGLUTININ (FRAGMENT).
GN BCSP.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
OX Fabales; Fabaceae; Papilionoideae; Glycine.
RN NCBI_TaxID=3847;
RP SEQUENCE FROM N.A.
RA Morasutti C., Marchetti S., De Amicis F., Zaina G., Zanetti M.;
RT "Expression and purification of the antimicrobial peptide SMAP-29 from
tobacco transgenic plants by SceVMA-intein system";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA De Amicis F.;
RL Thesis (1998), University of Udine, DPTVA.
DR EMBL: AJ276118; CAB83040.1; -.
FT NON_TER 62 62
FT NON_TER 62 62
SQ SEQUENCE 62 AA; 7158 MW; 10690D53F7700443 CRC64;

Query Match 100.0%; Score 53; DB 10; Length 62;
Best Local Similarity 19.0%; Pred. No. 89;
Matches 4; Conservative 17; Mismatches 0; Indels 0; Gaps 0;

OY 1 CXXXCXXXXXXXXXXCXXC 21
ID 38 CLOCSERDSYRNQACHARC 58

RESULT 6

ID Q41097 PRELIMINARY; PRT; 66 AA.
AC Q41097;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, last annotation update)
DE A615R PROTEIN.
GN A615R.
OS Parametium bursaria chlorella virus 1 (BCV-1).
OC Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Phycodnavirus.
OX NCBI_TaxID=10506;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98022962; PubMed=9356347;
RA Li Y., Lu Z., Sun L., Ropp S., Kutish G.F., Rock D.L., Van Etten J.L.;
RT "Analysis of 74 kb of DNA located at the right end of the 330-kb
chlorella virus BCV-1 genome.";

RL Virology 237:360-377(1997).
DR EMBL: U42580; AAC97026.1; -.
SQ SEQUENCE 66 AA; 7112 MM; 66F77F7A97A522FE CRC64;

Query Match Similarity	100.0%	Score 53;	DB 12;	Length 66;
Best Local Similarity	19.0%	Pred. No. 93;		
Matches 4;	Conservative 17;	Mismatches 0;	Indels 0;	Gaps 0;

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Qy      1 CXXXXXXXXXXXXXXCXXC 21
         |::|:::|:::|:::|
Db      28 CLGTCGTYLGLRLGTC 48
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RESULT	7			
ID	09V199	PRELIMINARY:	PRT:	72 AA.
AC	09V199;			
DT	01-MAY-2000 (T-EMBLrel_13, Created)			
DT	01-JUN-2000 (T-EMBLrel_13, Last sequence update)			
DT	01-JUN-2000 (T-EMBLrel_14, Last annotation update)			
DE	MST84D PROTEIN.			
GN	MST84D.			
OS	Drosophila melanogaster (Fruit fly).			
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;			
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
OC	Ephydroidea; Drosophilidae; Drosophila.			
OX	NCBI_TaxID=7227;			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BERKELEY.			
RC	MEDLINE=20196006; PubMed10731132.			
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,			
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,			
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,			
RA	Sultion G.G., Wortman J.R., Yandell M.D., Zheng Q., Chen L.X.,			
RA	Brandon R.C., Rogers Y.-H.C., Blasej R.G., Champe M., Pfeiffer B.D.,			
RA	Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Mkios G.L.G.,			
RA	Avril J.F., Agayuni A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,			
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,			
RA	Beeson K.Y., Benos P.V., Bereman B.P., Bhandari D., Bolshakov S.,			
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,			
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,			
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,			
RA	de Pablos B., Delcher A., Deng X., Mays A.D., Dew I., Dietz S.M.,			
RA	Dodson K., Doup L.E., Downes M., Dugan-Kocha S., Dunkov B.C., Dunn P.,			
RA	Dubin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,			
RA	Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,			
RA	Good A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,			
RA	Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Honck J.,			
RA	Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,			
RA	Jatani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,			
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,			
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,			
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,			
RA	Merkilov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,			
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,			
RA	Nelson D.R., Nelson K.A., Nixon K., Nussken D.R., Paetle J.M.,			
RA	Palazzo M., Pittman G.S., Pan S., Pollard J., Port V., Reese M.G.,			
RA	Reinert K., Remington K., Saunders R.D.C., Scheele F., Smith H.,			
RA	Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,			
RA	Spieler E., Spredling A.C., Stapleton M., Strong R., Sun E.,			
RA	Strickas R., Tector C., Turner C., Venter E., Wang A.H., Wang X.,			
RA	Wang Z.-Y., Wassman D.A., Weinstein G.M., Weissensbach J.,			
RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,			
RA	Ye J., Yen R.-F., Zaveri J.S., Zhu M., Zhang G., Zhao Q., Zheng L.,			
RA	Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,			
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,			
RT	"The genome sequence of <i>Drosophila melanogaster</i> ."			
RL	Science 287:2185-2195(2000).			
DR	EMBL: AE0031672; AAF54026.1; -			
DR	FLYBASE: Fgn0004175; Mst84d.			
DR	INTERPRO: IPR001450; -			

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DR PROSITE; PS00198; 4FE4S_FERREDOXIN; UNKNOWN_2.
SQ SEQUENCE 72 AA; 6840 MW; 8CE37449E5F88ABA CRC64;
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Query Match	100.0%;	Score 53;	DB 5;	length 72;
Best Local	Similarity	19.0%;	Pred. No. 98;	
Matches	4;	Conservative	17;	Mismatches 0; Indels 0; Gaps 0;

Qy	1	CXXXXX	21
Db	9	CCGPGCCGPGCCGPGCC	29

RESULT 8		PRELIMINARY;		PRT;		73 AA.	
ID	062554						
AC	062554;						
DT	01-AUG-1998 (TREMBLrel. 07, Created)						
DT	01-AUG-1998 (TREMBLrel. 07, Last sequence update)						
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)						
DE	METALOTHIONEIN 10 IB.						
OS	Mytilus edulis (Blue mussel).						
OC	Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea						
OC	Mytiloidea; Mytilidae; Mytilus.						
OX	NCBI_TaxID=6550;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RC	TISSUE=DIGESTIVE GLAND;						
RA	Barstye D., White K.N., Lovejoy D.A.;						
RL	Submitted (Apr-1998) to the EMBL/GenBank/DBJ databases.						
DR	EMBL; A0005452; CAA06549.1; -						
DR	INTERPRO: IPR000561; -						
DR	INTERPRO: IPR001008; -						
DR	INTERPRO: IPR003019; -						
DR	PPAM; PP00131; metalthio. 1.						
DR	PRINTS; PR00875; MTMOLUSC.						
DR	PROSITE; PS00022; EGF_1; UNKNOWN_1.						
SQ	SEQUENCE 73 AA; 7220 MW; 76797FB0FCDB3B2 CRC64;						
Query Match 100.0%; Score 53; DB 5; Length 73;							
Best Local Similarity 19.0%; Pred. No. 98;							
Matches 4; Conservative 17; Mismatches 0; Indels 0;							
QY	1 CXXXXXXXXXXXXXXXXXC 21						
Db	26 GCDACKAGADCKSCCKVVC 46						
RESULT 9							
ID	062555						
AC	062555;						
DT	01-AUG-1998 (TREMBLrel. 07, Created)						
DT	01-AUG-1998 (TREMBLrel. 07, Last sequence update)						
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)						
DE	METALOTHIONEIN 10 II.						
OS	Mytilus edulis (Blue mussel).						
OC	Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea						
OC	Mytiloidea; Mytilidae; Mytilus.						
OX	NCBI_TaxID=6550;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RC	TISSUE=DIGESTIVE GLAND;						
RA	Barstye D., White K.N., Lovejoy D.A.;						
RL	Submitted (Apr-1998) to the EMBL/GenBank/DBJ databases.						
DR	EMBL; A0005453; CAA06550.1; -						
DR	INTERPRO: IPR000561; -						
DR	INTERPRO: IPR001008; -						
DR	INTERPRO: IPR003019; -						
DR	PPAM; PP00131; metalthio. 1.						
DR	PRINTS; PR00875; MTMOLUSC.						
DR	PROSITE; PS00022; EGF_1; UNKNOWN_1.						

